

A Fully Connected Neural Network-Based Approach for Apple Disease Prediction via Environmental Sensors

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Abstract: Traditional manpower-based approaches to apple disease control face growing challenges due to the increased frequency of anomalous weather events, attributable to climate change, and labor shortages caused by aging rural populations. Specifically, the prevalence of high-temperature and high-humidity environments has led to a surge in domestic apple pests and diseases, resulting in significant economic losses and a sharp decline in total apple production. This paper proposes an AI-based prediction model that utilizes agro-meteorological data and a specialized dataset, focused on the "15-day window before and after the first precipitation," for the proactive forecasting of three major apple diseases: Marssonina blotch, White rot, and Anthracnose. The proposed method consistently demonstrated superior performance across all target diseases in terms of prediction accuracy, sensitivity, and specificity. Notably, the model achieved a sensitivity of 0.9750 for Anthracnose and a specificity of 0.9355 for White rot, validating its potential for practical on-farm application. This study is expected to advance eco-friendly precision agriculture by enabling farmers to optimize pest control timing and reduce unnecessary pesticide usage through the proactive prediction of disease outbreaks based on meteorological variations.

Keywords: Apple Disease Prediction; Fully Connected Neural Network; Environmental Sensors; AI; Climate

1. Introduction

Modern agriculture plays a pivotal role in global food security and the economy [1]. However, it currently faces complex challenges stemming from a declining agricultural population and climate change [2]. With the global population projected to reach approximately 9.7 billion by 2050, traditional farming methods are revealing critical limitations, including vulnerability to extreme weather events, resource depletion, and ecosystem degradation caused by excessive pesticide use [3]. Consequently, the transition to Precision Agriculture (PA)—which maximizes productivity with minimal resource input—has emerged as a global imperative to effectively respond to these changes and ensure agricultural sustainability [4].

In this context, Artificial Intelligence (AI) is increasingly gaining importance as a core technology for enhancing agricultural sustainability and productivity [5-7]. AI enables precision farming by meticulously analyzing and managing soil conditions, moisture levels, and nutrient requirements, thereby optimizing crop yields while minimizing resource waste [4], [8, 9]. Furthermore, AI-driven systems and automated machinery reduce labor costs and enhance operational efficiency, allowing for data-backed decisions on optimal sowing times and management strategies [10-12]. Crucially, AI supports farmers in making more accurate decisions amidst the uncertainties of climate change and pest outbreaks.

Apples, in particular, represent a major segment of the domestic fruit industry in South Korea, yet the sector is currently grappling with a severe crisis. While cultivation areas in Gyeongbuk and Chungbuk—traditionally the primary production hubs—have decreased, the cultivation limit has shifted northward, leading to an expansion of orchards in the Gangwon region [13]. In 2023, the total apple production plummeted to 394,000 tons, a sharp decline of approximately 30% compared to the previous year, due to compound climate

shocks such as low-temperature damage during the spring flowering season (frost and cold snaps) and heatwaves accompanied by heavy monsoon rains in the summer [14]. Moreover, as the aging rural population exacerbates labor shortages, traditional labor-intensive methods for pest control and disease surveillance have reached their structural limits [15].

To overcome these agricultural bottlenecks, Smart Farming, which integrates the Internet of Things (IoT), Big Data, and AI, is attracting significant attention as a new breakthrough. Historically, crop disease detection relied on visual inspections by experts or farmers, a process that was time-consuming, subjective, and difficult to scale for large-scale plantations. Currently, however, the analysis of vast amounts of image and environmental data collected via sensors, drones, and smartphones—using deep learning algorithms such as Convolutional Neural Networks (CNN) and Long Short-Term Memory (LSTM)—has enabled real-time pest identification and growth monitoring. This data-driven decision-making is revolutionizing agricultural practices from a reactive “treat-after-occurrence” approach to a proactive, predictive response system.

Specifically, apple disease prediction using AI is regarded as a key enabling technology for ensuring agricultural sustainability beyond simple automation. By learning from meteorological data—including temperature, humidity, precipitation, wind speed, and solar radiation—along with historical disease outbreaks, deep learning models can preemptively forecast the probability and risk levels of diseases even before symptoms become visible to the naked eye. Prediction-based precision control allows for the selective application of treatments only when and where necessary, providing environmental benefits such as reduced pesticide use and lower production costs, while preventing soil and water contamination.

In this paper, for the purpose of proactive control and prevention of apple disease transmission, we constructed a comprehensive training dataset by combining apple disease occurrence patterns surveyed by the Rural Development Administration (RDA) with agro-meteorological data (date, mean/max/min temperature, humidity, wind speed, precipitation, and solar radiation). Based on this dataset, we propose an AI model to predict the occurrence probability of three major diseases: Marssonina blotch, White rot, and Anthracnose, and evaluate its performance through various performance evaluations.

The remainder of this paper is organized as follows. Section II reviews related work and the theoretical background of the proposed technology. Section III describes the methodology for constructing the training dataset for apple disease prediction. Section IV details the design and implementation of the AI model based on agro-meteorological data. Section V demonstrates the superiority of the proposed model through diverse performance evaluation experiments. Finally, Section VI concludes the paper and suggests directions for future research.

2. Related Works

2.1 Apple Diseases

Figure 1 illustrates the primary diseases affecting apples: Marssonina blotch, White rot, and Anthracnose. Marssonina blotch, caused by a fungal pathogen, is one of the four most challenging apple diseases to control due to its ability to inflict fatal damage on leaves and trigger premature defoliation. This disease thrives in high-humidity conditions, specifically at temperatures between 20°C and 25°C with frequent rainfall (e.g., during the monsoon season). In South Korea, peak spore formation occurs twice a year—in early summer (May–June) and early autumn (September–October)—with rapid dispersal observed during prolonged wet periods following rain. Consequently, the risk of infection escalates significantly when leaves remain wet for more than 4 to 8 hours at temperatures around 20°C. Symptoms of Marssonina blotch typically manifest approximately 21 days after a rainfall event [16].

White rot (also known as Botryosphaeria canker) is caused by the pathogen *Botryosphaeria dothidea*. It inflicts severe damage on both the fruit and the branches (stems), causing concentric brown lesions on the fruit surface that lead to substantial quality degradation. The pathogen prefers relatively warm and humid climates, with an optimal growth temperature range of 28°C to 30°C (approximately 86°F). Spore infection requires the fruit surface to remain wet for a certain duration; notably, this required wetting time decreases as the temperature rises. Outbreaks are predominantly concentrated after September, during the late growth stage as the fruit matures. Under high-temperature conditions (above 24°C), the disease progresses rapidly, potentially rotting the entire fruit within a few days of infection. In controlled laboratory environments (22°C), the disease has been observed to manifest within 5 days [17].

Anthracoze, caused by fungi of the genus *Colletotrichum*, is a critical disease that leads to significant harvest losses by forming sunken brown lesions and pink spore masses on the fruit surface. Outbreaks are promoted by high-temperature and high-humidity environments (above 25°C) and tend to progress rapidly during the concentrated rainfall periods of summer [18]. Notably, it was observed that the likelihood of Anthracnose occurrence significantly increases when environmental conditions with temperatures of 24.2°C or higher and daily rainfall of at least 40mm persist for five consecutive days [19].



(a) Marssonina blotch



(b) White rot



(c) Anthracnose

Figure 1. Major Diseases of Apples

2.2 AI-Based Apple Disease Prediction Technology

Early detection and accurate classification of apple diseases are critical tasks directly linked to the enhancement of agricultural productivity. With recent advancements in computer vision and artificial intelligence (AI), diverse approaches have been extensively researched. This section systematically analyzes research trends, ranging from traditional machine learning-based methods to deep learning, real-time lightweight models, and hybrid attention-based architectures.

Initial studies on plant disease detection focused on combining hand-crafted feature extraction with machine learning classifiers. However, machine learning faces limitations due to its heavy reliance on explicit feature extraction in complex natural environments. To overcome this, Li et al. [20] proposed a bio-inspired framework that extracts regions of interest (ROI) via automatic K-means clustering and selects optimal color, texture, and shape features using the Ant Colony Optimization (ACO) algorithm, followed by classification

using a Support Vector Machine (SVM), achieving an accuracy of 92.50%. Meanwhile, non-destructive approaches have been attempted to detect latent infections before visual symptoms appear. Lee et al. [21] presented a method to identify morphological structural changes in internal leaf tissues during the early infection stages of apple blotch in the field by combining a non-invasive Optical Coherence Tomography (OCT) system with the Loop-mediated Isothermal Amplification (LAMP) technique.

The introduction of deep learning has led to the automation of feature extraction and a dramatic leap in classification accuracy. Dasari Rohith et al. [22] conducted a comparative analysis of various Convolutional Neural Network (CNN) architectures, including VGG, Inception, EfficientNet, MobileNet, and ResNet, demonstrating that ResNet—which effectively addresses the gradient vanishing problem through residual connections—achieved a peak validation accuracy of 98.9%. Research utilizing transfer learning to apply pre-trained models such as ResNet18, AlexNet, VGG16, and GoogLeNet to small-scale datasets has also been active, enhancing generalization performance [23]. Zhong and Zhao [24] utilized DenseNet-121 as a backbone and introduced a focal loss function and multi-label classification to address data imbalance, achieving 93.71% accuracy. For deployment in resource-constrained environments such as mobile devices, Vishnoi et al. [25] designed a lightweight 3-layer Convolutional Neural Network (Conv-3 DCNN) that significantly reduces computational burden while maintaining 98% accuracy.

For immediate response in orchard environments, real-time detection capabilities and model compression are essential. Jiang et al. [26] proposed the INAR-SSD model, which integrates Inception modules and rainbow concatenation into a Single Shot MultiBox Detector (SSD), achieving real-time diagnosis with a processing speed of 23.13 FPS and a mean Average Precision (mAP) of 78.80%. Khan et al. [27] confirmed the field applicability of apple disease detection in the Kashmir region by constructing a system that integrates an Xception-based classification model with detection models like Faster R-CNN, YOLOv4, and EfficientDet. Recently, to overcome the difficulty of detecting small lesions, Ai et al. [28] proposed AS-YOLOv11s, based on an improved YOLOv11s. By combining the ADown downsampling module, which prevents the loss of fine lesion textures, with a Spatial-Channel Synergy Attention (SCSA) mechanism, they reduced parameters and computation by 20.5% and 22.6%, respectively, while significantly improving detection accuracy for small-scale lesions.

To ensure robust performance in complex natural environments, recent research has evolved toward fusing multi-model ensembles with attention and Transformer structures. Turkoglu et al. [29] proposed an MLP-CNNs ensemble model that inputs features extracted from AlexNet, GoogLeNet, and DenseNet201 into an LSTM network and applies majority voting, achieving 99.2% classification accuracy. Navpreet and Roul [30] secured 99% accuracy while drastically shortening training time through the PCNN-IELM methodology, which passes features extracted by a pre-trained CNN to a Progressive Extreme Learning Machine (I-ELM) classifier. In attention-based research, Banjar et al. [31] proposed E-AppleNet, which integrates a Spatial-Channel Attention Module into EfficientNet-V2 to focus on key spatial and channel-wise features of lesions, demonstrating 99% classification performance. Yadav et al. [32] reported 98.7% accuracy in multi-class classification using AFD-Net, which applies the Swish activation function to the EfficientNet architecture. Furthermore, Srinivasan et al. [33] proposed DBA-ViNet, a dual-branch hybrid architecture that combines EfficientNetV2 for global morphological information and Swin Transformer for local fine lesion patterns via cross-attention. Through hierarchical feature fusion, this model achieved a classification accuracy of 99.51% even under complex background conditions.

3. Construction of Training Datasets for Apple Disease Prediction

In this study, training datasets were constructed by integrating apple disease occurrence patterns with agro-meteorological data from the surveyed regions. Table 1 presents a representative sample of the annual apple disease occurrence data provided by the Rural Development Administration (RDA) of South Korea. For instance, Survey Session 3 indicates the initial occurrence date of Marssonina blotch at Location A in 2023. While subsequent sessions (3 to 12) represent the spread of the disease at Location D, this study utilizes only the data from the 3rd session to capture the exact timing of the initial outbreak. Similarly, for the 2023 Anthracnose data at Location D, only the 6th survey session—marking the first occurrence—is included in the dataset.

Table 1. Representative sample of apple disease occurrence pattern data.

Date	address	Survey No.	No. of leaves infected with Marssonina blotch/640	Marssonina blotch prevalence	Number of fruits infected with Anthracnose/750	Anthracnose prevalence
20230517	A	1	0	0	0	0
20230601	A	2	0	0	0	0
20230615	A	3	1	0.2	0	0
20230701	A	4	2	0.3	0	0
20230716	A	5	50	7.8	0	0
20230801	A	6	100	15.6	2	0.3
20230816	A	7	200	31.3	1	0.1
20230903	A	8	200	31.3	100	13.3
20230910	A	9	300	46.9	100	13.3
20230916	A	10	300	46.9	150	20
20230923	A	11	450	70.3	150	20
20230930	A	12	400	62.5	0	0

Table 2 details the methodology for constructing training data to predict major apple diseases (Marssonina blotch, White rot, and Anthracnose). For example, the incubation period for Marssonina blotch is approximately 21 days. Accordingly, training data for predicting this disease was initially established based on agro-meteorological variables recorded over a 21-day period, including the date of the first rainfall event.

Table 2. Pseudo Code for Building the Apple Disease Learning Dataset

Module 1. Diseased Apple Training Data

- Step 1. Extract the survey date and latitude–longitude coordinates of locations where apple diseases occurred.
- Step 2. For each data point extracted in Step 1, identify the first date prior to the survey date when rainfall > 0.
- Step 3. If the disease is Marssonina blotch, set N to 21 days, and if the disease is White rot or Anthracnose, set N to 5 days.
- Step 4. Using the date extracted in Step 2 as the center, collect agricultural weather data for N days before and after, and combine it with the data extracted in Step 1.

Module 2. Healthy Apple Training Data

- Step 1. Extract agricultural weather data for the incubation period (15 days) prior to the date of healthy apples.
- Step 2. Combine the selected survey date, survey location, and occurrence-related information with the newly extracted agricultural weather data from Step 1.

The duration between infection and symptom manifestation in apple pathogens varies significantly across different diseases. For the early prediction of apple diseases, establishing a standardized and uniform framework for training data construction is essential. However, training datasets configured around the onset of symptoms, as shown in Table 2, inherently imply that the infection has already progressed. Therefore, this paper proposes a novel training model that integrates both the pre-symptomatic and symptomatic periods.

The incubation periods for various pathogens causing apple diseases typically range from 8 to 11 days [34]. Accordingly, using an 8-day incubation period as a baseline, we constructed a training dataset for disease prediction utilizing a 15-day window. As detailed in Table 3, this window encompasses the specific date of symptom onset along with a buffer of 7 days prior and 7 days after the event.

Table 3. Pseudo Code for Building the Learning Dataset for the proposed model

Module 1. Diseased Apple Training Data

- Step 1. Extract the survey date and latitude–longitude coordinates of locations where apple diseases occurred.
- Step 2. For each data point extracted in Step 1, identify the first date prior to the survey date when rainfall > 0.
- Step 3. Using the date extracted in Step 2 as the center, collect agricultural weather data for 7 days before and after, and combine it with the data extracted in Step 1.

Module 2. Healthy Apple Training Data

- Step 1. Extract agricultural weather data for the incubation period (15 days) prior to the date of healthy apples.
 - Step 2. Combine the selected survey date, survey location, and occurrence-related information with the newly extracted agricultural weather data from Step 1.
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4. Development and Optimization of AI Models for Apple Disease Prediction

In this study, the Optuna framework based on Bayesian Optimization was utilized to ensure the optimal performance of each disease prediction model. To perform a more sophisticated and extensive search than conventional hyperparameter tuning methods, the search space and iteration counts were expanded as follows:

- **Number of Optimization Trials:** Beyond the conventional 50 iterations, this study conducted 150 trials to increase the probability of converging to a global optimum.
- **Expansion of Hidden Layers and Nodes:** To sufficiently capture model complexity, the search range was broadened by increasing the maximum number of hidden layers from 4 to 6, and the maximum number of nodes per layer from 256 to 512.
- **Training Epochs:** The number of epochs was increased from the default 200 to 300 to ensure sufficient model convergence.

Through 150 optimization cycles via Optuna, the optimal model configurations for each disease and data construction criterion were derived as follows:

- **Marssonina blotch:** The 21-day incubation model exhibits a deep network structure with five hidden layers, as shown in Figure 2(a). It was configured to learn complex non-linear relationships by employing a mix of ReLU and Tanh activation functions. In contrast, the 15-day window model achieved optimal performance with a simplified structure consisting of a single hidden layer (128 nodes), as illustrated in Figure 2(b), while utilizing a high dropout rate (0.41) to prevent overfitting.

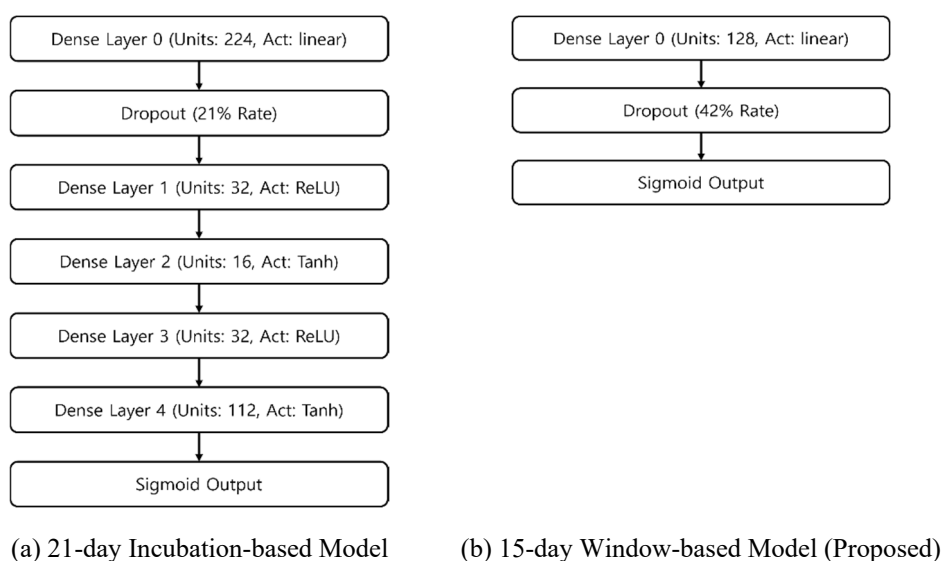


Figure 2. Architecture of the AI Model for Marssonina blotch Prediction

- **White rot:** The 5-day incubation model comprises two hidden layers (448 and 48 nodes), as shown in Figure 3(a), and performs learning through dense connections without dropout. The 15-day window model, illustrated in Figure 3(b), enhances generalization capability by combining three hidden layers with a dropout rate (0.22) and a batch size of 32.

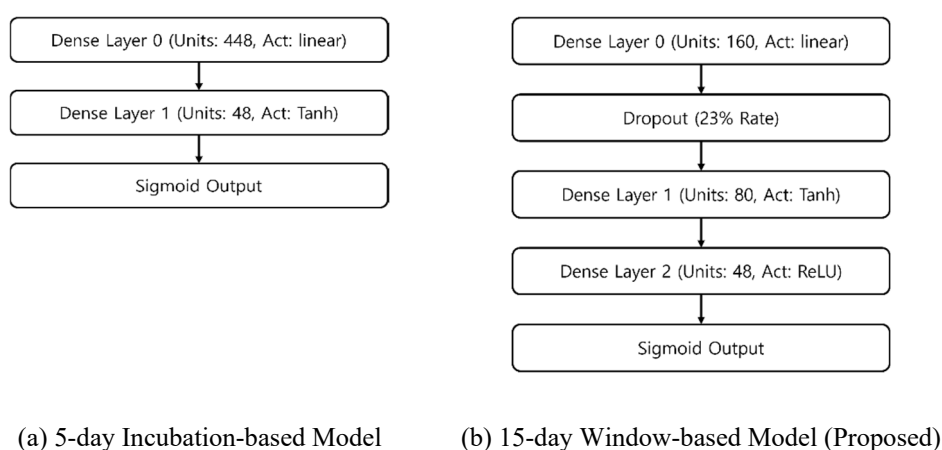


Figure 3. Architecture of the AI Model for White rot Prediction

- **Anthracnose:** The 5-day incubation model features a two-layer configuration, as shown in Figure 4(a), with a large-scale deployment of 512 nodes in the first layer to extract inter-variable features. The Tanh activation function was selected for this model. The 15-day window model, depicted in Figure 4(b), maintains a similar two-layer structure but employs the ReLU activation function and a batch size of 16 to facilitate more stable training.

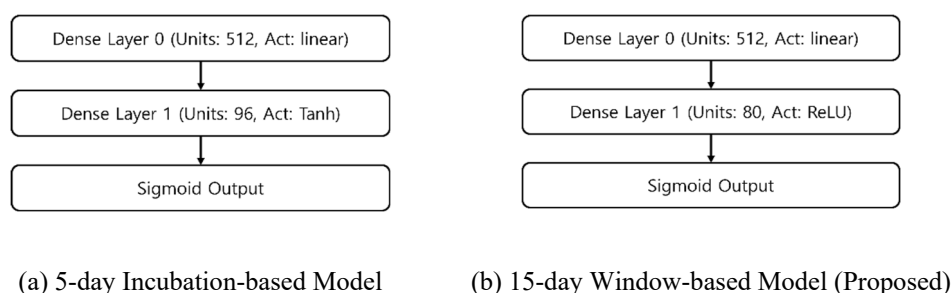


Figure 4. Architecture of the AI Model for Anthracnose Prediction

5. Performance Evaluation and Analysis Results

5.1 Dataset Characteristics and Evaluation Strategy for Spatial-Temporal Dependencies

To evaluate the proposed predictive model with high statistical rigor, we established a comprehensive dataset encompassing historical outbreak patterns of three major apple diseases—Marssonina blotch, White rot, and Anthracnose—spanning from 2013 to 2025, in collaboration with the Disaster Response Division of the Rural Development Administration(RDA). Agro-meteorological and plant pathology records often exhibit intense temporal and spatial autocorrelation, which can lead to overoptimistic performance metrics if data points are split randomly across identical timeframes or adjacent geographical areas. To strictly mitigate this spatial-temporal dependency and ensure realistic field-deployment validation, we adopted a rigorous strict-temporal splitting strategy(Out-of-Time Validation). Specifically, all historical records from 2013 to 2024 were designated as the training and internal validation framework, while the entirely independent data from the year 2025 was reserved exclusively as the prospective test set. This approach ensures that the model is evaluated on its ability to generalize to an unseen future production year under changing climatic trends, eliminating any temporal look-ahead bias. To address the class imbalance issues common in epidemiological models, the dataset was rigorously balanced with a 1:1 ratio of normal (healthy) and disease-conductive data points for each target illness. The detailed operational breakdown of the dataset size and partition is articulated as follows: (1) Training and Internal Validation Set (2013–2024): Marssonina blotch: 1,218 cases (609 normal, 609 disease), White rot: 582 cases (291 normal, 291 disease), Anthracnose: 944 cases (472 normal, 472 disease), (2) Independent Test Set (2025): Marssonina blotch: 90 cases (45 normal, 45 disease), White rot: 64 cases (32 normal, 32 disease), Anthracnose: 80 cases (40 normal, 40 disease). By evaluating the model on the completely decoupled 2025 dataset, we effectively controlled for spatial-temporal autocorrelation, presenting a robust estimation of model generalizability against annual climate variations.

5.2 Marssonina blotch

As depicted in Figure 5(a), for the dataset based on the 21-day incubation period, variables related to minimum temperature (mint) exhibited a strong positive correlation with disease occurrence. Specifically, the minimum temperatures during the initial outbreak stage, such as mint-1 and mint-2, recorded high correlation coefficients exceeding 0.7, identifying them as primary determinants of the disease. In contrast, in the dataset based on the 15-day window around the first precipitation, relative humidity (rh) related variables showed the most robust correlation, as shown in Figure 5(b). Variables such as rh-8, rh-7, and rh-9 ranked highest in correlation; this result is consistent with existing literature suggesting that humidity plays a decisive role in the dispersal and infection of Marssonina blotch spores.

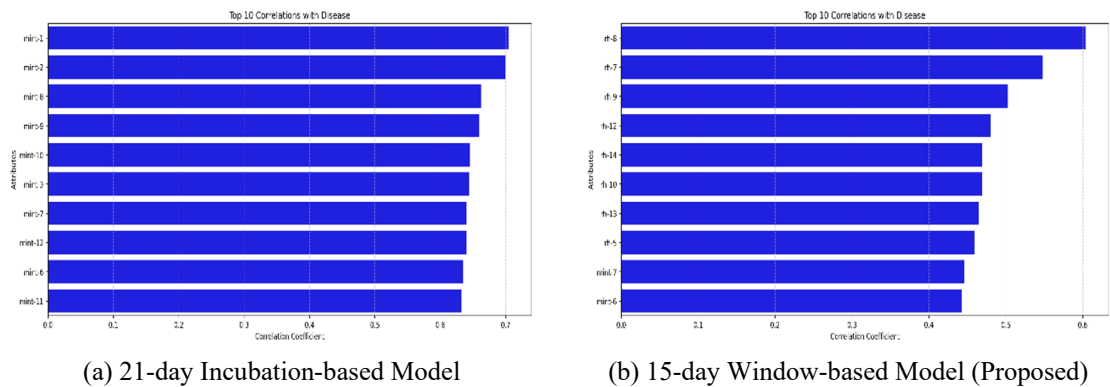


Figure 5. Correlation between Marssonina blotch Occurrence and Key Features

As illustrated in Figure 6 and Table 4, the validation loss of the 21-day incubation-based model converged through a gradual decline as training progressed, although some fluctuations were observed in certain intervals. The model demonstrated stable performance with a test accuracy of 0.9286.

In comparison, as shown in Figure 7 and Table 4, the proposed 15-day window model exhibited a rapid convergence rate, with the loss decreasing sharply in the early stages of training. Notably, it achieved high

learning efficiency, reaching a validation accuracy of approximately 0.98, and recorded a low error rate in final test performance (Loss: 0.2828).

The analysis reveals that while the overall accuracy was slightly higher in the 21-day incubation model, the proposed 15-day window model demonstrated superior performance in terms of Sensitivity (Recall), reaching 0.9333. This metric is particularly significant as it represents the model's ability to accurately detect actual disease occurrences without omission in real-world agricultural settings. Given that Marssonina blotch is exceedingly difficult to control once symptoms manifest, proactive and preventive intervention is essential. Therefore, the high-sensitivity 15-day window prediction model can serve as a more effective decision-making tool for farmers to preemptively block disease spread and minimize economic losses.

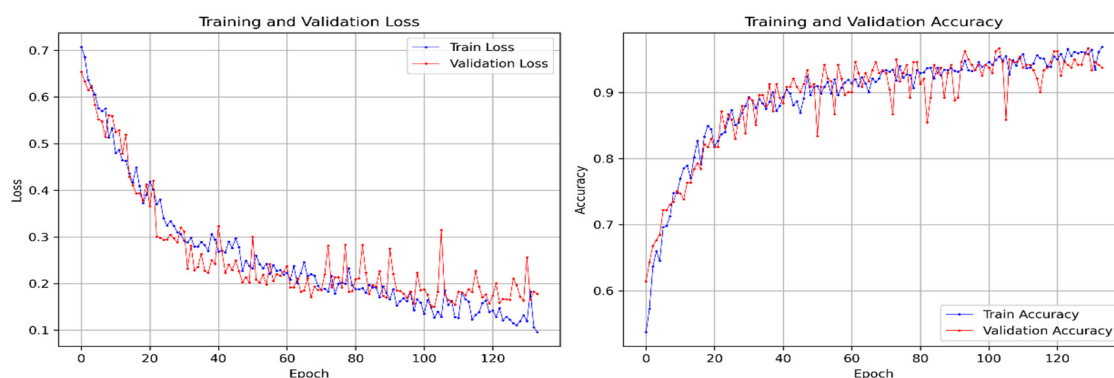


Figure 6. Training history of the Marssonina blotch prediction model based on a 21-day incubation period.

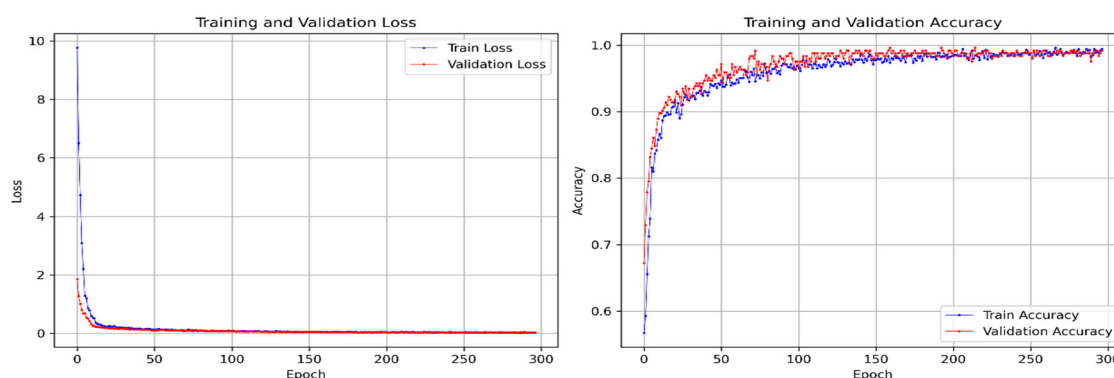


Figure 7. Training history of the proposed model based on a 15-day window around the first precipitation (Marssonina blotch).

Table 4. Comparison of prediction performance for Marssonina blotch AI models.

Evaluation Metrics	21-day Incubation Period	15-day Window (Proposed)
Test Accuracy	0.9286	0.9101
Test Loss	0.3040	0.2828
Sensitivity	0.9111	0.9333
Specificity	0.9487	0.8864

5.3 White rot

Analysis of meteorological factors revealed distinct differences in the core features learned by the models under the two different criteria. As illustrated in Figure 8(a), for the 5-day incubation-based criterion, relative humidity (rh-2, rh-1) and precipitation (precip-2) recorded 1 to 2 days prior to disease onset showed significant positive correlations. In contrast, the maximum temperature (maxt-2) exhibited a negative correlation. This suggests that a high-humidity environment immediately preceding the outbreak has a direct impact on symptom manifestation.

On the other hand, for the proposed 15-day window centered on the first precipitation, the majority of the top 10 attributes were related to relative humidity (rh), as shown in Figure 8(b). Specifically, humidity conditions surrounding the rainfall event, such as rh-8, rh-7, and rh-12, recorded high correlation coefficients exceeding 0.55, acting as robust leading indicators for disease occurrence. These findings strongly support the hypothesis of this study: that meteorological conditions prior to the incubation period exert a significant influence on the eventual outbreak of the disease.

The analysis of the training history for both models clearly demonstrates the disparity in learning efficiency based on the data construction range. As shown in Figure 9, the loss value for the 5-day incubation-based model declined gradually during the training process; however, the validation accuracy curve exhibited unstable fluctuations. This implies that a short data window of 5 days may provide insufficient information to fully capture the complex occurrence patterns of the disease.

In contrast, as depicted in Figure 10, the proposed 15-day window model showed a sharp decline in loss from the early stages of training, following a highly stable convergence curve. The close alignment and simultaneous rise of training and validation accuracy above 0.9 validate the superior generalization performance of the model.

The quantitative performance metrics for the White rot prediction AI models are summarized in Table 5. The proposed 15-day window model achieved a test accuracy of 0.9206, representing an approximately 10% performance improvement over the 5-day incubation-based model. Most notably, both the sensitivity and specificity of the proposed model exceeded 90%. This stands in stark contrast to the 5-day incubation model, which showed limitations in sensitivity (0.7812), proving that the proposed 15-day window model can identify the presence of the disease with a high degree of balance and accuracy.

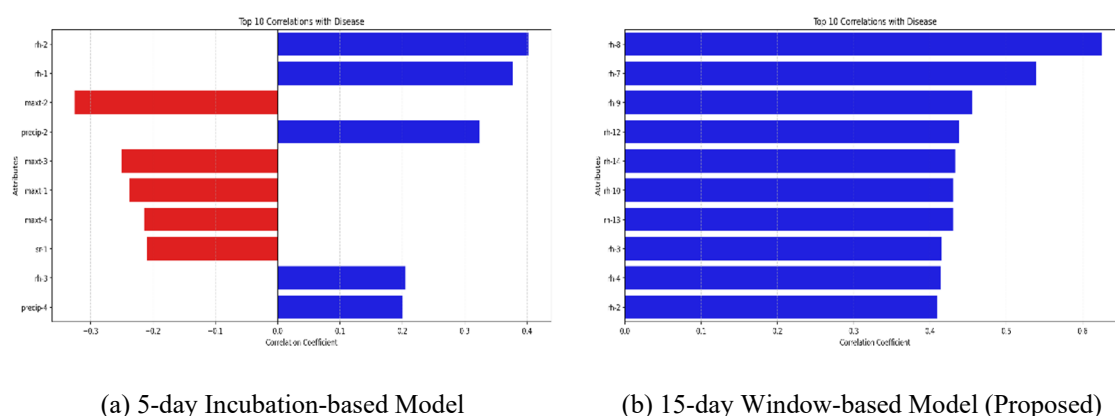


Figure 8. Correlation between white rot occurrence and key features.

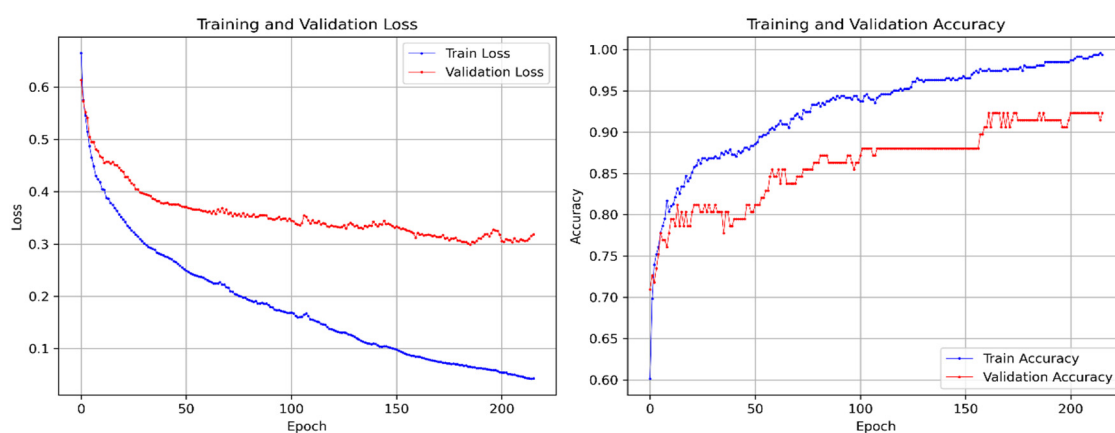


Figure 9. Training history of the white rot prediction model based on a 5-day incubation period.

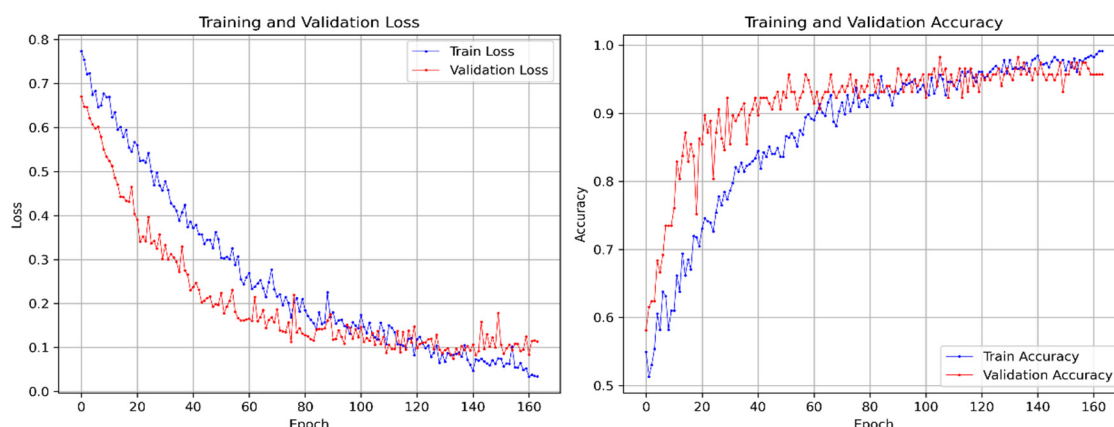


Figure 10. Training history of the proposed model based on a 15-day window around the first precipitation (white rot).

Table 5. Comparison of prediction performance for White rot AI models.

Evaluation Metrics	5-day Incubation Period	15-day Window (Proposed)
Test Accuracy	0.8254	0.9206
Test Loss	0.5023	0.1765
Sensitivity	0.7812	0.9062
Specificity	0.8710	0.9355

5.4 Anthracnose

Analysis of meteorological factors influencing Anthracnose occurrence revealed markedly contrasting correlation patterns depending on the data construction criteria. As shown in Figure 11(a), the dataset based on the 5-day incubation period involved a complex interaction of multiple variables; relative humidity (rh) and precipitation (precip) exhibited positive correlations, while maximum temperature (maxt) showed a negative correlation. Specifically, rh-2 and precip-2 ranked among the top features, suggesting that moisture conditions immediately preceding the outbreak are significant factors. In contrast, in the dataset based on the proposed 15-day window centered on the first precipitation, all top 10 attributes were related to relative humidity (rh), as illustrated in Figure 11(b). Led by rh-8, humidity factors throughout the analysis period consistently maintained strong positive correlations exceeding 0.5. This implies that the biological characteristic of Anthracnose in which spores are primarily dispersed by rain and host surface moisture is critical for infection—is more explicitly reflected in the proposed model.

A comparison of the training processes further highlights that the proposed 15-day window model achieved markedly superior results in terms of training stability and efficiency. As seen in Figure 12, the 5-day incubation-based model exhibited a widening error gap between training and validation data as training progressed, resulting in somewhat unstable convergence. Conversely, as shown in Figure 13, the 15-day window model demonstrated a steep decline in loss values from the early stages, with training and validation accuracies rising in close alignment, indicating high optimization performance. Notably, the stable maintenance of validation accuracy and the remarkably low final test loss of 0.1710 validate the model's excellent generalization capability.

The quantitative performance metrics for the Anthracnose prediction AI models are summarized in Table 6. The results indicate that the proposed 15-day window model significantly outperformed the baseline model in both test accuracy (0.9114) and loss values. Most remarkably, Sensitivity, the core metric for predicting disease outbreaks, reached 0.9750. This represents an improvement of more than 15% compared to the 5-day incubation model (0.8250), indicating that the proposed model can capture actual Anthracnose occurrences with near-perfect accuracy.

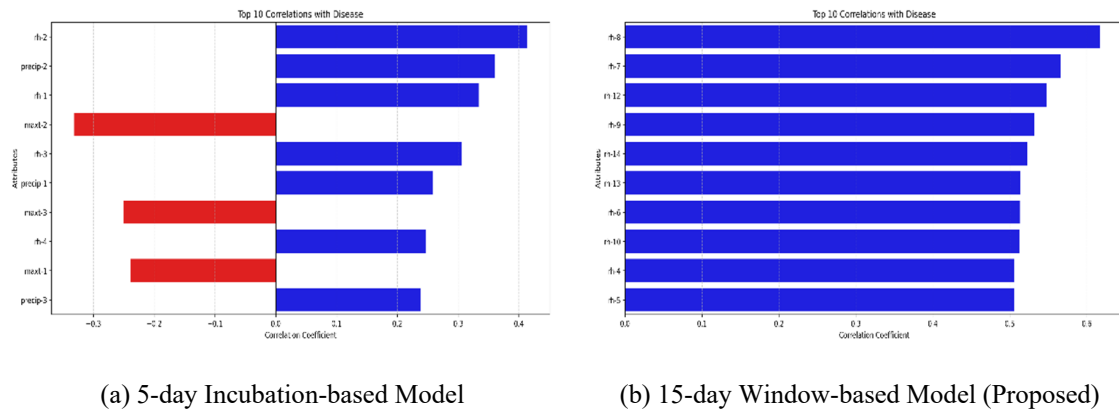


Figure 11. Correlation between Anthracnose occurrence and key features.

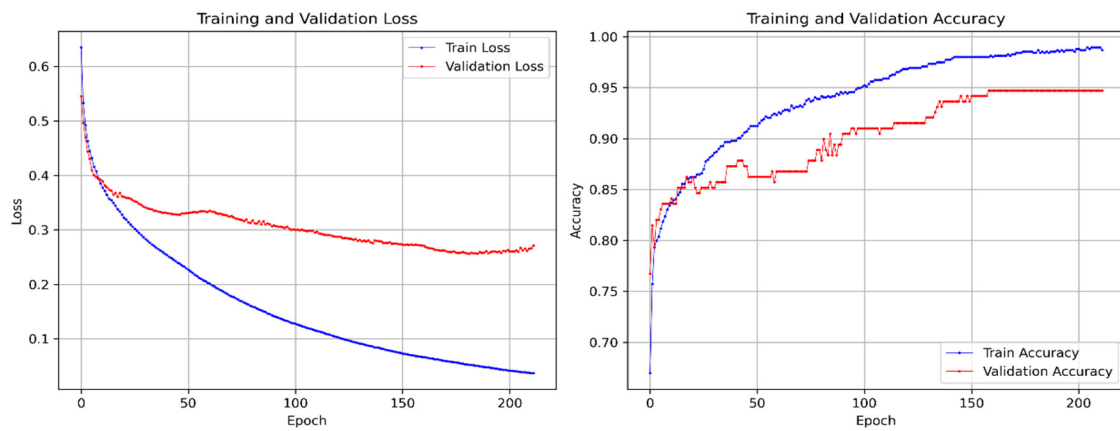


Figure 12. Training history of the Anthracnose prediction model based on a 5-day incubation period.

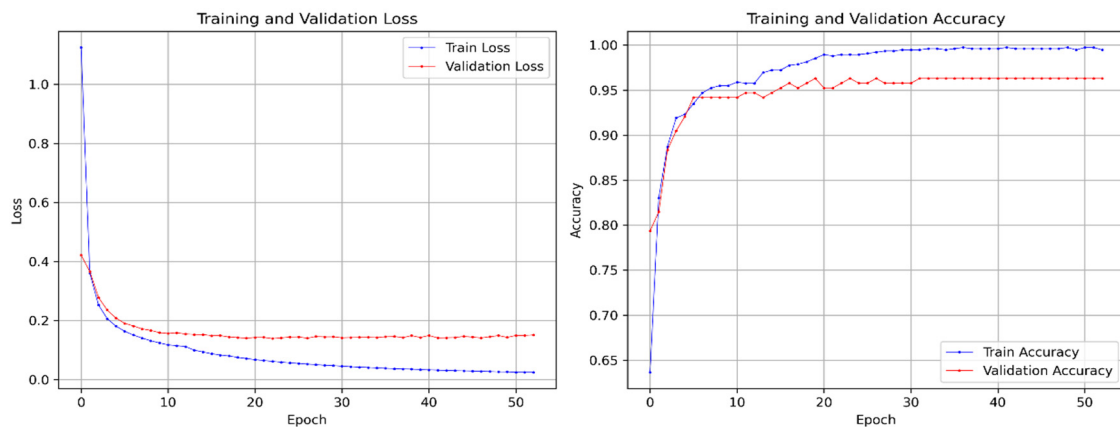


Figure 13. Training history of the proposed model based on a 15-day window around the first precipitation (Anthracnose).

Table 6. Comparison of prediction performance for Anthracnose AI models.

Evaluation Metrics	5-day Incubation Period	15-day Window (Proposed)
Test Accuracy	0.8608	0.9114
Test Loss	0.3148	0.1710
Sensitivity	0.8250	0.9750
Specificity	0.8974	0.8462

6. Conclusion and Future Work

In this paper, we proposed an AI-based prediction model utilizing agro-meteorological data to proactively forecast the three major apple diseases—Marssonina blotch, White rot, and Anthracnose—which have caused escalating damage in South Korea due to climate change. While conventional image-processing-based detection technologies are limited by their ability to identify diseases only after physical symptoms manifest, this study focused on recognizing the probability of outbreaks during the pre-incubation stage by analyzing meteorological factors that are intrinsically correlated with disease occurrence.

The experimental results demonstrated that the proposed training data construction method, centered on a “15-day window around the first precipitation,” consistently outperformed traditional datasets based on established incubation periods across all target diseases. These findings are significant as they extend beyond retrospective analysis of past occurrence patterns; by quantifying the likelihood of disease outbreaks in response to fluctuating meteorological conditions, this approach provides farmers with the optimal timing for proactive pest and disease control. In particular, the substantial improvement in Sensitivity—a critical metric for detecting disease outbreaks without omission—is expected to play a vital role in minimizing economic losses for agricultural households.

In future research, building upon the data construction and augmentation methodologies proposed in this study, we plan to further enhance model complexity and predictive precision. This will involve extending the proposed fully connected neural network infrastructure into hybrid architectures combined with advanced sequence and spatial models, such as Recurrent Neural Networks (RNN) or Transformers. Furthermore, we intend to expand the scope of this research to include a wider variety of fruit crops vulnerable to climate change. Ultimately, we aim to continue developing autonomous surveillance and control platforms that integrate with real-time agricultural weather monitoring systems, enabling farmers to receive instantaneous disease risk alerts via mobile devices for a more resilient agricultural ecosystem.

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